AMENDMENTS TO THE SPECIFICATION

Please **amend** the specification at page 12, after line 9 to expressly recite the following three paragraphs, which were incorporated by reference at the time of filing.

As recited in U.S. Patent No. 5,608,144, furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of between about 30 or 40 nucleotides and about 2,000 nucleotides should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of at least about 500 nucleotides is especially preferred.

As recited in U.S. Patent No. 4,563,417, any short sequence of bases (e.g., less than 6 bases), has a high degree of probability of being present in many nucleic acids. Thus, little or no specificity can be attained in hybridizations involving such short sequences. The present homologous probe sequence will be at least 10 bases, usually 20 bases or more, and preferably greater than 100 bases. From a practical standpoint, the homologous probe sequence will often be between 300-1000 nucleotides.

As recited in U.S. Patent Application Nos. 60/111,990, 09/459,109, and 09/459,110, polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) anaylsis. The SSCP technique is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in*

Molecular Medicine: Molecular Diagnosis of Genetic Diseases, Humana Press (1996); Orita *et al.*, *Genomics* 5:874-879 (1989).